

SEQUENCE LISTING

<110> Sauter, Margret M.
Lorbiecke, Rene

<120> ALTERATION OF GROWTH AND ADAPTION UNDER HYPOXIC
CONDITIONS

<130> CropDesign

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<170> PatentIn Ver. 2.1

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<222> (69)..(668)

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Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
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Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
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Val Ile Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
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00765739-1014601

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 Arg Ile Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
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 Tyr His Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
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 Leu Phe Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
 160 165 170

 cat ctt cct gca aga aag gag ttt ttg gct aaa ctt ctc aag tca gaa 638
 His Leu Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
 175 180 185 190

 ggt gaa aat caa gca gtt gaa ggc ttc tga gggttttgtt gggctcctgc 688
 Gly Glu Asn Gln Ala Val Glu Gly Phe
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 35 40 45
 Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn Leu Lys
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gtctgagagg tttcagag atg gag aac cag ttc cag gat ggc aag gag gag 171
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gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt 219
Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
15 20 25
cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca 267
Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
30 35 40
gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat 315
Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
45 50 55
gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg 363
Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
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Cys	Pro	Glu	Lys	Leu	Pro	Asn	Tyr	Glu	Ala	Lys	Leu	Lys	Asn	Phe	Phe
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Glu	Glu	His	Leu	His	Thr	Asp	Glu	Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly
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Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	Gln	Asn	Asp	Gln	Trp	Ile	Arg	Val
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Ala	Val	Lys	Lys	Gly	Gly	Met	Ile	Val	Leu	Pro	Ala	Gly	Met	Tyr	His
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Arg	Phe	Thr	Leu	Asp	Ser	Asp	Asn	Tyr	Ile	Lys	Ala	Met	Arg	Leu	Phe
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Val	Gly	Glu	Pro	Val	Trp	Thr	Pro	Tyr	Asn	Arg	Pro	His	Asp	His	Leu
				165					170					175	
Pro	Ala	Arg	Lys	Glu	Tyr	Val	Glu	Lys	Ile	Ile	Asn	Arg	Gly	Gly	Thr
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aac	gat	gag	gac	cag	agg	ctt	cct	cat	cac	cgt	gag	cca	aag	gaa	ttt	96
Asn	Asp	Glu	Asp	Gln	Arg	Leu	Pro	His	His	Arg	Glu	Pro	Lys	Glu	Phe	
			20					25					30			
gtg	tct	ctt	gac	aag	ctg	gct	gaa	ctt	gga	gtg	ctc	agc	tgg	aga	ctt	144
Val	Ser	Leu	Asp	Lys	Leu	Ala	Glu	Leu	Gly	Val	Leu	Ser	Trp	Arg	Leu	
		35					40					45				
gat	gct	gac	aat	tat	gag	act	gat	gag	gag	ttg	aag	aaa	att	cgg	gaa	192
Asp	Ala	Asp	Asn	Tyr	Glu	Thr	Asp	Glu	Glu	Leu	Lys	Lys	Ile	Arg	Glu	
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Asp	Arg	Gly	Tyr	Ser	Tyr	Ile	Asp	Phe	Cys	Glu	Val	Cys	Pro	Glu	Lys	
	65				70				75						80	
cta	ccg	aat	tac	gag	gag	aaa	atc	aag	aac	ttt	ttt	gaa	gaa	cac	ctg	288
Leu	Pro	Asn	Tyr	Glu	Glu	Lys	Ile	Lys	Asn	Phe	Phe	Glu	Glu	His	Leu	
				85					90					95		
cac	acc	gac	gag	gag	atc	cgt	tac	gct	gtt	gca	gga	agt	ggt	tac	ttt	336
His	Thr	Asp	Glu	Glu	Ile	Arg	Tyr	Ala	Val	Ala	Gly	Ser	Gly	Tyr	Phe	
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009799-021601

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Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
130 135 140

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Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
145 150 155 160

att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa 528
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
165 170 175

gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt 576
Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
180 185 190

aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt 631
Asn Ala Ala Ala
195

aataaatatt accatatggt ggcttttgctg ttcttgatgt gtgccttact aagcatgttt 691

aatgttgat tgtggcacta aataaatcac cccctatggg agattgattg tttatatgca 751

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35 40 45
Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
50 55 60
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
65 70 75 80
Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
85 90 95
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
100 105 110
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
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007530-0150

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gat	cag	cgg	cta	ccg	cac	cag	aag	aac	cca	ccg	gag	ttt	gtt	tca	gtg	95
Asp	Gln	Arg	Leu	Pro	His	Gln	Lys	Asn	Pro	Pro	Glu	Phe	Val	Ser	Val	
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Glu	Lys	Leu	Ala	Val	Ile	Gly	Val	Leu	Tyr	Trp	Lys	Leu	Asn	Pro	Asn	
			35					40					45			
gat	tac	gag	aac	gat	gaa	gaa	ttg	aaa	aaa	att	cgt	caa	agt	aga	ggc	191
Asp	Tyr	Glu	Asn	Asp	Glu	Glu	Leu	Lys	Lys	Ile	Arg	Gln	Ser	Arg	Gly	
		50					55					60				
tac	agc	tac	atg	gac	ttg	ctg	gat	ttg	tgc	cct	gag	aag	gtg	gat	aac	239
Tyr	Ser	Tyr	Met	Asp	Leu	Leu	Asp	Leu	Cys	Pro	Glu	Lys	Val	Asp	Asn	
	65				70					75						
tat	gag	cag	aag	ttg	aaa	aat	ttc	tat	acg	gag	cac	ata	cac	gca	gat	287
Tyr	Glu	Gln	Lys	Leu	Lys	Asn	Phe	Tyr	Thr	Glu	His	Ile	His	Ala	Asp	
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Glu	Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	
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gac	aag	gat	gat	cgc	tgg	att	cgc	atc	tgg	atg	aag	gcc	ggg	gat	atg	383
Asp	Lys	Asp	Asp	Arg	Trp	Ile	Arg	Ile	Trp	Met	Lys	Ala	Gly	Asp	Met	
			115					120					125			
att	gtc	ttg	cct	gct	ggg	att	tac	cac	cgg	ttc	acc	cta	gat	act	gat	431
Ile	Val	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp	
		130					135					140				

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Asn	Tyr	Val	Lys	Leu	Met	Arg	Leu	Phe	Val	Gly	Glu	Pro	Val	Trp	Thr	
145						150					155					
cct	tac	aat	cga	cca	caa	gaa	gat	cat	cca	gca	agg	aag	gag	tac	atc	527
Pro	Tyr	Asn	Arg	Pro	Gln	Glu	Asp	His	Pro	Ala	Arg	Lys	Glu	Tyr	Ile	
160					165					170					175	
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Lys	Ser	Val	Thr	Glu	Arg	Val	Gly	Val	Pro	Leu	Thr	Ala	His			
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Lys	Leu	Ala	Val	Ile	Gly	Val	Leu	Tyr	Trp	Lys	Leu	Asn	Pro	Asn	Asp	
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Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	
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Val	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp	Asn	
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Tyr	Val	Lys	Leu	Met	Arg	Leu	Phe	Val	Gly	Glu	Pro	Val	Trp	Thr	Pro	
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0928E23-0450


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gat caa aga ctc ccc cac cac aaa gaa ccc aag gag ttt gtc tcg ttg 148
Asp Gln Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser Leu
25 30 35

gac caa ctt gct gaa ctt gga gtc ctt agc tgg aaa cta gat gct gat 196
Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala Asp
40 45 50 55

aac cat gaa aat gat cca gag ctg aag aag att cgt gaa gag cgt ggt 244
Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
60 65 70

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Tyr	Thr	Tyr	Met	Asp	Val	Cys	Glu	Val	Cys	Pro	Glu	Lys	Leu	Pro	Asn	
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Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val Arg
105 110 115

gat cgc aat gaa gct tgg att cgt gtg tgg gtc aag aaa gga gga atg 436
Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
120 125 130 135

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Ile	Ile	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Glu	Ser	
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Lys Arg Glu Glu Val Ile Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu		
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gat cag agg ctt cct cat cac cgt gaa cct aag gaa tat gta tcc ttg	149	
Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Tyr Val Ser Leu		
	25 30 35	
gat aaa ctt gct gag ctt gga gta ctc agc tgg cga ttg gat gct gat	197	
Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu Asp Ala Asp		
	40 45 50 55	
aac tat gaa aat gat gaa gag ttg aag aaa att cgt gaa gaa cga ggt	245	
Asn Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly		
	60 65 70	
tac tcc tac atg gac ttc tgc gag gtt tgc cct gag aag ctt cca aat	293	
Tyr Ser Tyr Met Asp Phe Cys Glu Val Cys Pro Glu Lys Leu Pro Asn		
	75 80 85	
tat gag gag aag ata aaa aat ttc ttc gaa gaa cat att cat act gat	341	
Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Ile His Thr Asp		
	90 95 100	
gag gag atc cgt tac tgt gtg gca gga agt ggt tat ttt gat gta cgg	389	
Glu Glu Ile Arg Tyr Cys Val Ala Gly Ser Gly Tyr Phe Asp Val Arg		
	105 110 115	
gat cat aat gat aaa tgg att cgt gtg tgg gtg aag aaa gga ggc atg	437	
Asp His Asn Asp Lys Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met		
	120 125 130 135	
ata gtt tta cct gct gga att tat cat cgc ttt act ctg gat aca gac	485	
Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp		
	140 145 150	
aac tat att aag gca atg cgg ctc ttt gtt ggt gat cca att tgg act	533	
Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro Ile Trp Thr		
	155 160 165	

ccg tac aat cgt ccg cac gat cat ctt cct gca agg aag gag tat atc 581
Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
170 175 180

aag aac ttt ttg cgg gag gaa ggt ggt ggc caa gcc gtt gat gct gcc 629
Lys Asn Phe Leu Arg Glu Glu Gly Gly Gly Gln Ala Val Asp Ala Ala
185 190 195

gca taa aatcaacatt catctggtgg tggccaagtc gttgatgctg ccgcataaaa 685
Ala
200

tcagcattca tctctggtat cgtgtcttat aaaatatgaa accccggatt tgtggtaata 745

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Ser	Trp	Arg	Leu	Asp	Ala	Asp	Asn	Tyr	Glu	Asn	Asp	Glu	Glu	Leu	Lys
	50					55					60				
Lys	Ile	Arg	Glu	Glu	Arg	Gly	Tyr	Ser	Tyr	Met	Asp	Phe	Cys	Glu	Val
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Cys	Pro	Glu	Lys	Leu	Pro	Asn	Tyr	Glu	Glu	Lys	Ile	Lys	Asn	Phe	Phe
				85					90					95	
Glu	Glu	His	Ile	His	Thr	Asp	Glu	Glu	Ile	Arg	Tyr	Cys	Val	Ala	Gly
			100					105					110		
Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	His	Asn	Asp	Lys	Trp	Ile	Arg	Val
		115					120					125			
Trp	Val	Lys	Lys	Gly	Gly	Met	Ile	Val	Leu	Pro	Ala	Gly	Ile	Tyr	His
	130					135					140				
Arg	Phe	Thr	Leu	Asp	Thr	Asp	Asn	Tyr	Ile	Lys	Ala	Met	Arg	Leu	Phe
	145				150					155				160	
Val	Gly	Asp	Pro	Ile	Trp	Thr	Pro	Tyr	Asn	Arg	Pro	His	Asp	His	Leu
				165					170					175	
Pro	Ala	Arg	Lys	Glu	Tyr	Ile	Lys	Asn	Phe	Leu	Arg	Glu	Glu	Gly	Gly
			180					185					190		
Gly	Gln	Ala	Val	Asp	Ala	Ala	Ala								
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 <212> DNA
 <213> Human

<220>
 <221> CDS
 <222> (1)..(564)

<400> 13

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Arg	Thr	Arg	His	Pro	His	Cys	Ala	Ser	Val	Val	Gln	Ala	Trp	Tyr	Met	
1				5					10					15		
gac	gac	gcc	ccg	ggc	acc	cgc	ggc	aac	ccc	acc	gcc	ccg	acc	ccg	gcc	96
Asp	Asp	Ala	Pro	Gly	Thr	Arg	Gly	Asn	Pro	Thr	Ala	Pro	Thr	Pro	Ala	
			20					25					30			
gcc	cag	tgc	gct	gga	gca	gct	gcg	cgg	ctc	ggg	gtg	ctc	tac	tgg	aag	144
Ala	Gln	Cys	Ala	Gly	Ala	Ala	Ala	Arg	Leu	Gly	Val	Leu	Tyr	Trp	Lys	
		35					40					45				
ctg	gat	gct	gac	aaa	tat	gag	aat	gat	cca	gaa	tta	gaa	aag	atc	cga	192
Leu	Asp	Ala	Asp	Lys	Tyr	Glu	Asn	Asp	Pro	Glu	Leu	Glu	Lys	Ile	Arg	
	50					55					60					
aga	gag	agg	aac	tac	tcc	tgg	atg	gac	atc	ata	acc	ata	tgc	aaa	gat	240
Arg	Glu	Arg	Asn	Tyr	Ser	Trp	Met	Asp	Ile	Ile	Thr	Ile	Cys	Lys	Asp	
65					70				75					80		
aaa	cta	cca	aat	tat	gaa	gaa	aag	att	aag	atg	ttc	tac	gag	gag	cat	288
Lys	Leu	Pro	Asn	Tyr	Glu	Glu	Lys	Ile	Lys	Met	Phe	Tyr	Glu	Glu	His	
			85						90					95		
ttg	cac	ttg	gac	gat	gag	atc	cgc	tac	atc	ctg	gat	ggc	agt	ggg	tac	336
Leu	His	Leu	Asp	Asp	Glu	Ile	Arg	Tyr	Ile	Leu	Asp	Gly	Ser	Gly	Tyr	
			100					105					110			
ttc	gat	gtg	agg	gac	aag	gag	gac	cag	tgg	atc	cgg	atc	ttc	atg	gag	384
Phe	Asp	Val	Arg	Asp	Lys	Glu	Asp	Gln	Trp	Ile	Arg	Ile	Phe	Met	Glu	
		115					120					125				
aag	gga	gac	atg	gtg	acg	ctc	ccc	gcg	ggg	atc	tat	cac	cgc	ttc	acg	432
Lys	Gly	Asp	Met	Val	Thr	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	
	130					135					140					
gtg	gac	gag	aag	aac	tac	acg	aag	gcc	atg	cgg	ctg	ttt	gtg	gga	gaa	480
Val	Asp	Glu	Lys	Asn	Tyr	Thr	Lys	Ala	Met	Arg	Leu	Phe	Val	Gly	Glu	
145					150				155						160	
ccg	gtg	tgg	aca	gcg	tac	aac	cgg	ccc	gct	gac	cat	ttt	gaa	gcc	cgc	528
Pro	Val	Trp	Thr	Ala	Tyr	Asn	Arg	Pro	Ala	Asp	His	Phe	Glu	Ala	Arg	
				165					170					175		

ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgcctgcc 574
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
180 185

tgggaactaa cacgtgcctc gtaaaggctc ccaatgtaat gaactgagca gaaaattcaa 634
tcaactttct ctttgctttt agaggatagc cttgaggtag attatctttc ctttgtaaga 694
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attgcattca ggttgagtcc caaatgaaag tttcatctcc cgaaatgcag ttccttagat 874
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<212> PRT
<213> Human

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Ala Gln Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
35 40 45
Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
50 55 60
Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
65 70 75 80
Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
85 90 95
Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr
100 105 110
Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
115 120 125
Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
130 135 140
Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu
145 150 155 160
Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
165 170 175
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
180 185

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 <211> 972
 <212> DNA
 <213> Mouse

<220>
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 <222> (17)..(556)

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 Asp Pro Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu
 15 20 25

gag cag ctg cgc acg ctc gga gtg ctc tat tgg aag cta gat gct gac 148
 Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp
 30 35 40

gag tat gag aac gat cca gaa cta gaa aag atc cgg aaa atg aga aac 196
 Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn
 45 50 55 60

tac tcc tgg atg gac atc atc acc ata tgc aaa gat aca ctt ccc aat 244
 Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn
 65 70 75

tac gag gag aag atc aag atg ttc ttt gag gaa cat ctg cat ctg gat 292
 Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu Asp
 80 85 90

gag gag atc cgc tac atc ctg gag ggt agt ggg tac ttc gat gtc agg 340
 Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
 95 100 105

gac aag gag gac aag tgg atc cgg att tcc atg gag aag ggg gac atg 388
 Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met
 110 115 120

att act ctt cct gcc ggc atc tat cac cgc ttc aca ctg gac gag aag 436
 Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys
 125 130 135 140

aat tac gtg aag gcc atg cgg ctg ttt gtt gga gaa cct gtg tgg aca 484
 Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr
 145 150 155

cca tac aac cgg cca gct gac cat ttt gat gcc cgt gta cag tac atg 532
 Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met
 160 165 170

agt ttt ttg gaa gga aca gca tag cagtgtcct caaagagaaa actgcactgt 586
 Ser Phe Leu Glu Gly Thr Ala
 175 180

gtgaatctcc tgctgtggta accgaatgga aagttgctca cttttctgct tttgtatttg 646
 aacttgaggg tagactagct ctcttttgcta ggattgtgag atcagtgtct tttaaatgaa 706
 agcctctcta aaagtgagtt ttacatggaa gccacaaaaa tgtgaaaaag tgaccttaat 766
 tttccctaac tgtcaagact tagaggtata ggagccctgg attggtatgt gcattcatgc 826
 atggccaatc ttcattctccc agatcttttag gtgtctgttg gtgtgaagct atgcctcctg 886
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 <211> 179
 <212> PRT
 <213> Mouse

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 20 25 30
 Leu Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala
 35 40 45
 Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg
 50 55 60
 Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro
 65 70 75 80
 Asn Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu
 85 90 95
 Asp Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val
 100 105 110
 Arg Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp
 115 120 125
 Met Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu
 130 135 140
 Lys Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp
 145 150 155 160
 Thr Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr
 165 170 175
 Met Ser Phe Leu Glu Gly Thr Ala
 180


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<220>  
<221> CDS  
<222> (36) .. (581)
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Ctg agc ccg aat cag ccc gtc agc gtc cag cag ctg gag cac atc gga 149
 Leu Ser Pro Asn Gln Pro Val Ser Val Gln Gln Leu Glu His Ile Gly
 25 30 35

ctg cag aag atc cga gag gag aag ggt tat tcc ttt atg gac atc ata 245
Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr Ser Phe Met Asp Ile Ile
55 60 65 70

ttt	tac	gaa	gag	cat	ctc	cac	ctg	gac	gat	gag	atc	cgt	tat	att	ctg	341
Phe	Tyr	Glu	Glu	His	Leu	His	Leu	Asp	Asp	Glu	Ile	Arg	Tyr	Ile	Leu	
		90						95					100			

cga ata gcg gtg tct aaa ggc gac ctc atc act tta ccg gcc ggg att 437
Arg Ile Ala Val Ser Lys Gly Asp Leu Ile Thr Leu Pro Ala Gly Ile
120 125 130

ctg ttc gtg ggt gaa ccc gtc tgg aag gcc tac aac cgt cca gcc gat 533
Leu Phe Val Gly Glu Pro Val Trp Lys Ala Tyr Asn Arg Pro Ala Asp
155 160 165

gac ttt gac atc cgc aag gaa tac gtg aac tcg ctg gga agc tcc tga 581
 Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn Ser Leu Gly Ser Ser
 170 175 180

aatgcctgat gggattgatt tagtgctgag aatcagactc tgcggtgcct tanacagaca 641
 ngcagcaata gtagagctaa catgtcatta cttagtcatc aagacacacc tgatataaag 701
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<210> 18
 <211> 181
 <212> PRT
 <213> Zebrafish

<400> 18
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 Gln Arg Leu Pro His Lys Leu Ser Pro Asn Gln Pro Val Ser Val Gln
 20 25 30
 Gln Leu Glu His Ile Gly Val Phe His Trp Lys Leu Asn Ala Asp Ile
 35 40 45
 Tyr Glu Asn Asp Pro Glu Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr
 50 55 60
 Ser Phe Met Asp Ile Ile Thr Ile His Pro Asp Lys Leu Pro Asp Tyr
 65 70 75 80
 Gln Asn Lys Leu Lys Met Phe Tyr Glu Glu His Leu His Leu Asp Asp
 85 90 95
 Glu Ile Arg Tyr Ile Leu Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp
 100 105 110
 Glu Gly Asp Arg Trp Ile Arg Ile Ala Val Ser Lys Gly Asp Leu Ile
 115 120 125
 Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp Glu Ser Asn
 130 135 140
 Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Lys Ala
 145 150 155 160
 Tyr Asn Arg Pro Ala Asp Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn
 165 170 175
 Ser Leu Gly Ser Ser
 180